WEST Search History

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DATE: Friday, February 25, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ	
☐	L30	l25 and l5	1
☐	L29	l25 and l4	1
☐	L28	L27 and l18	6
☐	L27	L26 and l1	36
☐	L26	l23 or l24	7864
☐	L25	(ferrone or wang or hsu).in.	35918
☐	L24	(424/184.1, 130.1)![CCLS]	0
☐	L23	(530/300,327,328,387.1)![CCLS]	7864
☐	L22	L2 and L18	1
☐	L21	L20.clm.	3
☐	L20	anti-gd3	86
☐	L19	L18 and L15	46
☐	L18	mimetic or peptidomimetic	21512
☐	L17	GD3 with peptidomimetic	0
☐	L16	GD3 with peptid$	37
☐	L15	gd3 with ganglioside	354
☐	L14	gd3 ganglioside	130
☐	L13	L12 and L11	39
☐	L12	inhibit$	572024
☐	L11	L10 and L5	60
☐	L10	L9 or L8	55343
☐	L9	L6.clm.	36700
☐	L8	L6.ab.	35568
☐	L7	L6 and L5	77
☐	L6	antibod$	138401
☐	L5	L4 or L3 or L2	94
☐	L4	L1.clm.	62
☐	L3	L1.ab.	39
☐	L2	L1.ti.	14
☐	L1	gd3	666

END OF SEARCH HISTORY

Application Number	Application No.	Applicant(s)
‖‖‖‖‖‖‖‖‖‖‖‖‖ (barcode)	10/618,336	FERRONE ET AL.
	Examiner	Art Unit
	Brandon J Fetterolf, PhD	1642

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Search | PubMed | for | #16 AND #5 | Preview/Index History Clipboard Details | [Preview] [Go] [Clear]

- Click on query # to add to strategy
- Search numbers may not be continuous; all searches are represented.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search History will be lost after eight hours of inactivity.

Field: **Author, Limits: Publication Date to 2002**

☑ Limits

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	Time	Result
#18 Search #16 AND #5 Field: Author, Limits: **Publication Date to 2002**	11:39:21	29
#16 **Related Articles** for PubMed (Select 10499418)	11:37:13	143
#15 Search #14 AND #5 Field: Author, Limits: **Publication Date to 2002**	11:36:21	1
#14 Search willers Field: Author, Limits: **Publication Date to 2002**	11:35:23	355
#13 Search #12 ND #5 Limits: **Publication Date to 2002**	10:28:49	0
#12 Search mimetic Field: All Fields, Limits: **Publication Date to 2002**	10:28:34	3142
#11 Search #10 AND #5 Field: Title/Abstract, Limits: **Publication Date to 2002**	10:28:21	0
#10 Search peptidomimetic Field: **Title/Abstract, Limits: Publication Date to 2002**	10:28:09	553
#9 Search #5 and #8 Field: Title/Abstract, Limits: **Publication Date to 2002**	10:27:38	0
#8 Search mimetic Field: **Title/Abstract, Limits: Publication Date to 2002**	10:27:27	3108
#7 Search #3 Field: **Title/Abstract, Limits: Publication Date to 1998**	10:24:43	38
#6 Search #3 and #5 Field: Title/Abstract	10:24:29	0
#5 Search GD3 Field: Title/Abstract	10:24:18	1809
#4 Search GD3 Field: Author	10:24:08	0
#3 Search #1 AND #2 Field: Author	10:23:56	49
#2 Search faki Field: Author	10:23:48	1509
#1 Search ishikawa Field: Author	10:23:40	13940

Clear History

Feb 23 2005 11:00:20

(FILE 'HOME' ENTERED AT 14:03:56 ON 25 FEB 2005)

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        FILE 'CANCERLIT' ENTERED AT 14:04:06 ON 25 FEB 2005
L1          641 S GD3
L2        14360 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?
L3       194977 S ANTIGEN?
L4         8188 S IMMUNOGEN?
L5       162627 S ANTIBOD?
L6           82 S ANTI-GD3
L7           20 S L1 AND L2
L8           10 S L7 AND L4
L9           10 S L8 AND L5
L10           5 S L9 AND L3
L11           5 S L10 NOT PY>2002

        FILE 'MEDLINE' ENTERED AT 14:07:05 ON 25 FEB 2005
L12        1813 S GD3
L13       63707 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?
L14      595321 S ANTIGEN?
L15       32569 S IMMUNOGEN?
L16      680887 S ANTIBOD?
L17          62 S L12 AND L13
L18          26 S L17 AND L16
L19          10 S L18 AND L15
L20           6 S L19 NOT PY>2002

        FILE 'CAPLUS' ENTERED AT 14:09:21 ON 25 FEB 2005
L21        6468 S GD3
L22           0 S FERRONE/AU
L23       64212 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?
L24      357467 S ANTIGEN?
L25       29966 S IMMUNOGEN?
L26      426207 S ANTIBOD?
L27          77 S L21 AND L23
L28          29 S L27 AND L26
L29           9 S L28 AND L25
L30           6 S L29 AND (ANTI()GD3)

        FILE 'PCTFULL' ENTERED AT 14:11:47 ON 25 FEB 2005
L31         600 S GD3
L32       37018 S MIMIC? OR MIMETIC? OR PEPTIDOMIMETIC?
L33          13 S L31/AB
L34         107 S L31/CLM
L35          34 S L31 (S) L32
L36          14 S L35 AND L34
L37       75273 S ANTIBOD?
L38        3750 S L32/CLM
L39           9 S L38 AND L36
L40           0 S L39 AND L33
L41           9 S L39 AND L37
L42           4 S L41 NOT PY>2002
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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:04:47 ; Search time 24 Seconds
                                         (without alignments)
                                         37.325 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
   No.   Score   Match Length DB ID   Description
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     1   41   58.6   90   4 US-09-358-383C-31   Sequence 31, Appl
     2   41   58.6   960   4 US-09-694-777A-21   Sequence 21, Appl
     3   41   58.6   962   4 US-09-614-480-9   Sequence 9, Appli
     4   41   58.6   962   4 US-09-694-777A-3   Sequence 3, Appli
     5   41   58.6   962   4 US-09-694-777A-24   Sequence 24, Appl
     6   41   58.6   962   4 US-10-422-075-9   Sequence 9, Appli
     7   41   58.6   987   4 US-09-694-777A-22   Sequence 22, Appl
     8   41   58.6   988   4 US-09-614-480-2   Sequence 2, Appli
     9   41   58.6   988   4 US-10-162-012-5   Sequence 5, Appli
    10   41   58.6   988   4 US-10-162-012-12   Sequence 12, Appl
    11   41   58.6   988   4 US-10-422-075-2   Sequence 2, Appli

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12      41      58.6     989   4   US-09-694-777A-4          Sequence 4, Appli
13      41      58.6     989   4   US-09-694-777A-23         Sequence 23, Appl
14      40      57.1      96   4   US-09-403-343B-24         Sequence 24, Appl
15      39      55.7     166   4   US-09-252-991A-24322      Sequence 24322, A
16      38      54.3     103   4   US-09-252-991A-28978      Sequence 28978, A
17      38      54.3    2500   2   US-08-801-263A-2          Sequence 2, Appli
18      38      54.3    2500   3   US-09-102-248-2           Sequence 2, Appli
19      38      54.3    2500   4   US-09-367-764-2           Sequence 2, Appli
20      38      54.3    2517   2   US-08-801-263A-5          Sequence 5, Appli
21      38      54.3    2517   3   US-09-102-248-5           Sequence 5, Appli
22      38      54.3    2517   4   US-09-367-764-5           Sequence 5, Appli
23      37      52.9     250   4   US-09-270-767-61069       Sequence 61069, A
24      37      52.9     433   4   US-09-270-767-45556       Sequence 45556, A
25      37      52.9     534   4   US-09-270-767-46023       Sequence 46023, A
26      37      52.9    3830   4   US-09-693-205A-4          Sequence 4, Appli
27      36      51.4      42   4   US-09-270-767-31926       Sequence 31926, A
28      36      51.4      42   4   US-09-270-767-47143       Sequence 47143, A
29      36      51.4     200   4   US-09-252-991A-18742      Sequence 18742, A
30      36      51.4     256   4   US-09-949-016-7576        Sequence 7576, Ap
31      36      51.4     256   4   US-09-949-016-7577        Sequence 7577, Ap
32      36      51.4     280   4   US-09-949-016-9249        Sequence 9249, Ap
33      36      51.4     280   4   US-09-949-016-9250        Sequence 9250, Ap
34      36      51.4     306   4   US-09-270-767-41758       Sequence 41758, A
35      36      51.4     330   3   US-09-188-930-125         Sequence 125, App
36      36      51.4     330   4   US-09-312-283C-125        Sequence 125, App
37      36      51.4     404   3   US-09-191-608-18          Sequence 18, Appl
38      36      51.4     431   4   US-09-270-767-57907       Sequence 57907, A
39      36      51.4     443   4   US-09-266-965-131         Sequence 131, App
40      36      51.4     447   3   US-09-191-608-19          Sequence 19, Appl
41      36      51.4     471   3   US-09-191-608-17          Sequence 17, Appl
42      36      51.4     497   3   US-09-191-608-20          Sequence 20, Appl
43      36      51.4     555   4   US-09-270-767-42597       Sequence 42597, A
44      36      51.4     617   3   US-09-188-930-303         Sequence 303, App
45      36      51.4     617   4   US-09-312-283C-303        Sequence 303, App
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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:37:08 ; Search time 354 Seconds
                                        (without alignments)
                                        11.093 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
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            3:   /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
            4:   /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
            5:   /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
            6:   /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
            7:   /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
            8:   /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
            9:   /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
           10:   /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
           11:   /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
           12:   /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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           19:   /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
           20:   /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	62.9	47	15	US-10-424-599-193456	Sequence 193456,
2	44	62.9	296	15	US-10-210-281-4	Sequence 4, Appli
3	44	62.9	307	15	US-10-210-281-6	Sequence 6, Appli
4	44	62.9	329	15	US-10-112-944-313	Sequence 313, App
5	44	62.9	351	15	US-10-333-572-3	Sequence 3, Appli
6	42	60.0	312	15	US-10-282-122A-51764	Sequence 51764, A
7	42	60.0	344	14	US-10-017-161-1954	Sequence 1954, Ap
8	42	60.0	344	15	US-10-292-798-1602	Sequence 1602, Ap
9	41	58.6	90	14	US-10-185-867-31	Sequence 31, Appl
10	41	58.6	263	16	US-10-437-963-164408	Sequence 164408,
11	41	58.6	648	16	US-10-322-696-33	Sequence 33, Appl
12	41	58.6	960	14	US-10-188-308-21	Sequence 21, Appl
13	41	58.6	960	14	US-10-188-296-21	Sequence 21, Appl
14	41	58.6	960	14	US-10-188-341-21	Sequence 21, Appl
15	41	58.6	960	14	US-10-188-297-21	Sequence 21, Appl
16	41	58.6	962	14	US-10-188-308-3	Sequence 3, Appli
17	41	58.6	962	14	US-10-188-308-24	Sequence 24, Appl
18	41	58.6	962	14	US-10-188-296-3	Sequence 3, Appli

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19      41      58.6     962    14    US-10-188-296-24          Sequence 24, Appl
20      41      58.6     962    14    US-10-188-341-3           Sequence 3, Appli
21      41      58.6     962    14    US-10-188-341-24          Sequence 24, Appl
22      41      58.6     962    14    US-10-188-297-3           Sequence 3, Appli
23      41      58.6     962    14    US-10-188-297-24          Sequence 24, Appl
24      41      58.6     962    14    US-10-174-613-4           Sequence 4, Appli
25      41      58.6     962    14    US-10-174-613-5           Sequence 5, Appli
26      41      58.6     962    15    US-10-422-075-9           Sequence 9, Appli
27      41      58.6     987    14    US-10-188-308-22          Sequence 22, Appl
28      41      58.6     987    14    US-10-188-296-22          Sequence 22, Appl
29      41      58.6     987    14    US-10-188-341-22          Sequence 22, Appl
30      41      58.6     987    14    US-10-188-297-22          Sequence 22, Appl
31      41      58.6     988    10    US-09-875-321-5           Sequence 5, Appli
32      41      58.6     988    10    US-09-875-321-12          Sequence 12, Appl
33      41      58.6     988    14    US-10-128-323-2           Sequence 2, Appli
34      41      58.6     988    14    US-10-162-012-5           Sequence 5, Appli
35      41      58.6     988    14    US-10-162-012-12          Sequence 12, Appl
36      41      58.6     988    14    US-10-174-613-2           Sequence 2, Appli
37      41      58.6     988    14    US-10-174-613-3           Sequence 3, Appli
38      41      58.6     988    15    US-10-369-022-18          Sequence 18, Appl
39      41      58.6     988    15    US-10-422-075-2           Sequence 2, Appli
40      41      58.6     988    15    US-10-162-102-5           Sequence 5, Appli
41      41      58.6     988    15    US-10-162-102-12          Sequence 12, Appl
42      41      58.6     988    15    US-10-332-447-31          Sequence 31, Appl
43      41      58.6     988    16    US-10-322-696-36          Sequence 36, Appl
44      41      58.6     988    17    US-10-916-061-5           Sequence 5, Appli
45      41      58.6     988    17    US-10-916-061-12          Sequence 12, Appl
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 06:41:39 ; Search time 129 Seconds
                                            (without alignments)
                                            152.212 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
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                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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                    Maximum Match 100%
                    Listing first 45 summaries

Command line parameters:
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99
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336_@CGN_1_1_177_@runat_18022005_145631_15147 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7


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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                                  SUMMARIES
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			% Query				
Result	No.	Score	Match	Length	DB	ID	Description
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c	2	51	72.9	162841	4	US-09-949-016-13733	Sequence 13733, A
c	3	47	67.1	2487	4	US-09-573-080A-80	Sequence 80, Appl
c	4	47	67.1	86936	4	US-09-949-016-17314	Sequence 17314, A
	5	46	65.7	767677	4	US-09-949-016-12147	Sequence 12147, A
	6	46	65.7	767677	4	US-09-949-016-17361	Sequence 17361, A
	7	45	64.3	292	4	US-09-602-565-19	Sequence 19, Appl
	8	45	64.3	299	4	US-09-602-565-18	Sequence 18, Appl
	9	45	64.3	502	4	US-09-602-565-9	Sequence 9, Appli
	10	45	64.3	548	4	US-09-602-565-10	Sequence 10, Appl
	11	45	64.3	577	4	US-09-602-565-11	Sequence 11, Appl
	12	45	64.3	601	4	US-09-949-016-136449	Sequence 136449,
c	13	45	64.3	6063	1	US-08-195-744-4	Sequence 4, Appli
c	14	45	64.3	6063	2	US-08-788-279-4	Sequence 4, Appli
c	15	45	64.3	17488	4	US-09-949-016-15574	Sequence 15574, A
c	16	44	62.9	601	4	US-09-949-016-53650	Sequence 53650, A
c	17	44	62.9	601	4	US-09-949-016-140101	Sequence 140101,
	18	44	62.9	601	4	US-09-949-016-156494	Sequence 156494,
	19	44	62.9	7376	4	US-09-949-016-4052	Sequence 4052, Ap
	20	44	62.9	12225	4	US-09-949-016-17360	Sequence 17360, A
c	21	44	62.9	91538	4	US-09-949-016-15703	Sequence 15703, A
	22	44	62.9	123513	4	US-09-949-016-15794	Sequence 15794, A
c	23	44	62.9	160759	4	US-09-949-016-16514	Sequence 16514, A

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c  24        44     62.9 231129    4   US-09-949-016-16110        Sequence 16110, A
   25        44     62.9 250715    4   US-09-949-016-13294        Sequence 13294, A
c  26        44     62.9 266293    4   US-09-949-016-11934        Sequence 11934, A
   27        44     62.9 536165    4   US-09-214-808-1            Sequence 1, Appli
   28        44     62.9 678533    4   US-09-949-016-14577        Sequence 14577, A
   29        44     62.9 678533    4   US-09-949-016-14578        Sequence 14578, A
   30        43     61.4    695    5   PCT-US93-06251-21          Sequence 21, Appl
   31        43     61.4   1188    4   US-09-270-767-12519        Sequence 12519, A
   32        43     61.4   4810    3   US-09-596-824-5            Sequence 5, Appli
   33        43     61.4   4810    4   US-09-885-329-5            Sequence 5, Appli
c  34        43     61.4   6158    4   US-09-919-497-6            Sequence 6, Appli
   35        43     61.4   6453    1   US-08-306-691B-14          Sequence 14, Appl
   36        43     61.4   6453    3   US-09-209-668-10           Sequence 10, Appl
   37        43     61.4   6453    3   US-09-356-952-8            Sequence 8, Appli
c  38        43     61.4  45755    4   US-09-949-016-15889        Sequence 15889, A
   39        43     61.4  47799    4   US-09-949-016-13363        Sequence 13363, A
   40        43     61.4  64518    4   US-09-949-016-17289        Sequence 17289, A
   41        43     61.4 194915    4   US-09-949-016-15584        Sequence 15584, A
   42      42.5     60.7    601    4   US-09-949-016-21607        Sequence 21607, A
   43      42.5     60.7    601    4   US-09-949-016-21608        Sequence 21608, A
   44      42.5     60.7    601    4   US-09-949-016-142272       Sequence 142272,
   45      42.5     60.7    601    4   US-09-949-016-142273       Sequence 142273,
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 07:39:25 ; Search time 380 Seconds
                                              (without alignments)
                                              186.647 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145632_15239/app_query.fasta_1.1
99
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10618336_@CGN_1_1_678_@runat_18022005_145632_15239
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
     No.   Score   Match   Length DB   ID   Description
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        1   53   75.7   790 17   US-10-012-697-38   Sequence 38, Appl
  c   2   51   72.9   613 18   US-10-357-930-19541   Sequence 19541, A
  c   3   51   72.9   658 18   US-10-357-930-49337   Sequence 49337, A
        4   51   72.9   674 13   US-10-027-632-235370   Sequence 235370,
        5   51   72.9   674 13   US-10-027-632-235371   Sequence 235371,
        6   51   72.9   674 17   US-10-027-632-235370   Sequence 235370,
        7   51   72.9   674 17   US-10-027-632-235371   Sequence 235371,
  c   8   47   67.1   418 10   US-09-918-995-11767   Sequence 11767, A
  c   9   47   67.1   2487 10   US-09-854-867-80   Sequence 80, Appl
       10   46   65.7   940 15   US-10-017-161-1389   Sequence 1389, Ap
       11   46   65.7   943 15   US-10-017-161-1385   Sequence 1385, Ap
  c   12   46   65.7   979   9   US-09-925-300-690   Sequence 690, App

	13	46	65.7	13654	17	US-10-292-798-1131	Sequence 1131, Ap
	14	46	65.7	47804	15	US-10-017-161-717	Sequence 717, App
	15	46	65.7	47804	17	US-10-292-798-629	Sequence 629, App
c	16	45	64.3	290	18	US-10-425-115-34478	Sequence 34478, A
	17	45	64.3	299	15	US-10-280-953-13	Sequence 13, Appl
	18	45	64.3	300	18	US-10-425-115-156755	Sequence 156755,
	19	45	64.3	362	18	US-10-767-701-22224	Sequence 22224, A
	20	45	64.3	502	15	US-10-280-953-9	Sequence 9, Appli
c	21	45	64.3	520	16	US-10-029-386-1283	Sequence 1283, Ap
	22	45	64.3	671	18	US-10-767-701-6366	Sequence 6366, Ap
c	23	45	64.3	702	15	US-10-156-761-7433	Sequence 7433, Ap
c	24	45	64.3	752	18	US-10-425-115-28784	Sequence 28784, A
	25	45	64.3	871	18	US-10-425-115-174480	Sequence 174480,
c	26	45	64.3	27007	9	US-09-764-868-1424	Sequence 1424, Ap
c	27	45	64.3	31477	13	US-10-087-192-373	Sequence 373, App
c	28	45	64.3	155937	18	US-10-723-860-2208	Sequence 2208, Ap
	29	45	64.3	158405	14	US-10-175-523-86	Sequence 86, Appl
	30	45	64.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	31	44	62.9	142	17	US-10-424-599-50614	Sequence 50614, A
c	32	44	62.9	350	18	US-10-357-930-14433	Sequence 14433, A
c	33	44	62.9	386	18	US-10-357-930-35543	Sequence 35543, A
c	34	44	62.9	386	18	US-10-357-930-44355	Sequence 44355, A
c	35	44	62.9	390	17	US-10-424-599-2370	Sequence 2370, Ap
	36	44	62.9	543	10	US-09-764-891-1368	Sequence 1368, Ap
	37	44	62.9	543	10	US-09-764-891-7744	Sequence 7744, Ap
c	38	44	62.9	600	13	US-10-027-632-141934	Sequence 141934,
c	39	44	62.9	600	13	US-10-027-632-141935	Sequence 141935,
c	40	44	62.9	600	13	US-10-027-632-141936	Sequence 141936,
c	41	44	62.9	600	17	US-10-027-632-141934	Sequence 141934,
c	42	44	62.9	600	17	US-10-027-632-141935	Sequence 141935,
c	43	44	62.9	600	17	US-10-027-632-141936	Sequence 141936,
c	44	44	62.9	605	18	US-10-021-323-1034	Sequence 1034, Ap
c	45	44	62.9	888	14	US-10-198-846-3405	Sequence 3405, Ap

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OM protein - protein search, using sw model

Run on: February 23, 2005, 04:36:07 ; Search time 74 Seconds
                                          (without alignments)
                                          62.718 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   44   62.9   121   4   AAB95737   Aab95737 Human pro
     2   44   62.9   296   8   ADJ50939   Adj50939 Human nov
     3   44   62.9   307   8   ADJ50941   Adj50941 Human nov
     4   44   62.9   329   8   ADM87220   Adm87220 Human pro
     5   44   62.9   351   5   AAE18955   Aae18955 Human cel
     6   44   62.9   351   8   ADN01129   Adn01129 Human cel
     7   42   60.0   262   3   AAG43457   Aag43457 Arabidops
     8   42   60.0   262   3   AAG23843   Aag23843 Arabidops
     9   42   60.0   312   6   ABU23840   Abu23840 Protein e

10	42	60.0	344	7	ADC87149	Adc87149 Human GPC
11	42	60.0	351	3	AAG23842	Aag23842 Arabidops
12	42	60.0	351	3	AAG43456	Aag43456 Arabidops
13	42	60.0	381	3	AAG43455	Aag43455 Arabidops
14	42	60.0	381	3	AAG23841	Aag23841 Arabidops
15	41	58.6	90	6	ABU61687	Abu61687 Program d
16	41	58.6	90	7	ADB66818	Adb66818 Potassium
17	41	58.6	348	1	AAP94682	Aap94682 Human man
18	41	58.6	648	8	ADQ59397	Adq59397 Human can
19	41	58.6	856	7	ABW01409	Abw01409 Human HEA
20	41	58.6	962	3	AAY49944	Aay49944 Human pot
21	41	58.6	988	4	AAB31714	Aab31714 A human a
22	41	58.6	988	4	AAE01043	Aae01043 Human eth
23	41	58.6	988	5	ABG70999	Abg70999 Human tra
24	41	58.6	988	5	ABB76165	Abb76165 Human pot
25	41	58.6	988	5	AAO14214	Aao14214 Human tra
26	41	58.6	988	7	ADC77655	Adc77655 Human 334
27	41	58.6	988	7	ABW01364	Abw01364 Human pot
28	41	58.6	988	8	ADQ59400	Adq59400 Human can
29	41	58.6	989	3	AAY49945	Aay49945 Human pot
30	41	58.6	989	7	ADC77667	Adc77667 Human 332
31	41	58.6	989	8	ADR44914	Adr44914 Polypepti
32	41	58.6	1174	4	ABB65304	Abb65304 Drosophil
33	40	57.1	59	8	ABO56119	Abo56119 Human gen
34	40	57.1	84	4	AAU63085	Aau63085 Propionib
35	40	57.1	84	6	ABM59604	Abm59604 Propionib
36	40	57.1	699	8	ABO84631	Abo84631 Mouse can
37	40	57.1	1178	8	ADP74025	Adp74025 Murine CD
38	39	55.7	85	4	AAU21335	Aau21335 Human nov
39	39	55.7	103	4	AAU59241	Aau59241 Propionib
40	39	55.7	103	6	ABM55760	Abm55760 Propionib
41	39	55.7	166	7	ABO75576	Abo75576 Pseudomon
42	39	55.7	194	3	AAG61086	Aag61086 Arabidops
43	39	55.7	194	3	AAG56099	Aag56099 Arabidops
44	39	55.7	198	3	AAG56098	Aag56098 Arabidops
45	39	55.7	198	3	AAG61085	Aag61085 Arabidops

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 06:38:09 ; Search time 2602 Seconds
                                        (without alignments)
                                        223.468 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0

```
                    Delop    6.0 , Delext    7.0

Searched:          4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145630_15121/app_query.fasta_1.1
99
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336_@CGN_1_1_4200_@runat_18022005_145630_15121 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7


Database :       GenEmbl:*
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                 3:   gb_in:*
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                               SUMMARIES
                        %
Result                  Query
    No.    Score  Match Length DB  ID                          Description
    --------------------------------------------------------------------------
        1     54   77.1  10465  1  AE008241                    AE008241 Agrobacte
c   2     54   77.1  13358  1  AE009373                    AE009373 Agrobacte
        3     53   75.7    864  6  AX540791                    AX540791 Sequence
        4     53   75.7  35447  2  AC007181                    AC007181 Homo sapi
        5     53   75.7  39972  2  AC087250                    AC087250 Homo sapi
```

c	6	53	75.7	146534	9	AC092143	AC092143 Homo sapi
c	7	53	75.7	193729	4	AC129099	AC129099 Canis fam
c	8	53	75.7	202454	2	AC128934	AC128934 Rattus no
c	9	53	75.7	210446	9	AC133919	AC133919 Homo sapi
	10	53	75.7	235804	2	AC106639	AC106639 Rattus no
c	11	53	75.7	261914	2	AC122581	AC122581 Rattus no
	12	53	75.7	348283	2	AC125706	AC125706 Rattus no
c	13	52	74.3	193041	10	AC110169	AC110169 Mus muscu
	14	52	74.3	277112	2	AC131428	AC131428 Rattus no
c	15	51	72.9	613	6	CQ487674	CQ487674 Sequence
	16	51	72.9	616	11	BV053434	BV053434 S212P6035
c	17	51	72.9	658	6	CQ517470	CQ517470 Sequence
	18	51	72.9	97101	2	AL450308	AL450308 Homo sapi
	19	51	72.9	106341	9	AL390316	AL390316 Human DNA
c	20	51	72.9	130878	9	AL450063	AL450063 Human DNA
	21	51	72.9	164485	2	AC025340	AC025340 Homo sapi
c	22	51	72.9	167218	2	AC069041	AC069041 Homo sapi
	23	51	72.9	176161	2	AC021173	AC021173 Homo sapi
	24	51	72.9	185953	10	AC123872	AC123872 Mus muscu
	25	51	72.9	215326	9	AC091160	AC091160 Homo sapi
	26	51	72.9	216400	2	AC125934	AC125934 Rattus no
c	27	51	72.9	216601	2	AC129691	AC129691 Rattus no
c	28	51	72.9	218618	10	AL928587	AL928587 Mouse DNA
	29	51	72.9	237855	2	AC136663	AC136663 Rattus no
	30	51	72.9	244238	2	AC131627	AC131627 Rattus no
	31	51	72.9	250663	2	AC134905	AC134905 Mus muscu
c	32	51	72.9	258792	2	AC135491	AC135491 Rattus no
	33	50	71.4	39089	4	AF483210	AF483210 Canis fam
	34	50	71.4	110000	2	AC096220_1	Continuation (2 of
c	35	50	71.4	212129	2	AC139817	AC139817 Homo sapi
	36	50	71.4	219683	2	AC103126	AC103126 Rattus no
	37	50	71.4	222587	2	AC109744	AC109744 Rattus no
	38	50	71.4	242510	2	AC128507	AC128507 Rattus no
c	39	49	70.0	110000	2	AC091343_0	AC091343 Rattus no
c	40	49	70.0	148965	2	AC136069	AC136069 Rattus no
c	41	49	70.0	151881	9	AC008629	AC008629 Homo sapi
c	42	49	70.0	171011	10	AC140244	AC140244 Mus muscu
c	43	49	70.0	174203	2	AC141570	AC141570 Rattus no
c	44	49	70.0	174640	2	AC017044	AC017044 Homo sapi
c	45	49	70.0	176427	2	AC151671	AC151671 Gallus ga

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 06:37:39 ; Search time 361 Seconds
                                    (without alignments)
                                    196.778 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5

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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:      8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145629_15113/app_query.fasta_1.1
99
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336_@CGN_1_1_644_@runat_18022005_145629_15113 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      N_Geneseq_16Dec04:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                        %
Result                  Query
    No.   Score   Match Length DB  ID                        Description
    ----------------------------------------------------------------------
      1      53    75.7    790   9  ADB81726                  Adb81726 Human cDN
      2      53    75.7    864   6  ABQ88782                  Abq88782 Human pro
c   3      51    72.9    613   5  ABV19550                  Abv19550 Human pro
c   4      51    72.9    658   5  ABV49318                  Abv49318 Human pro
```

c	5	47	67.1	418	9	ACH24555	Ach24555 Human adu
c	6	47	67.1	2487	7	ADS31047	Ads31047 Human gen
c	7	46	65.7	303	6	AAS98123	Aas98123 Human DNA
c	8	46	65.7	979	3	AAF16255	Aaf16255 Human pro
c	9	46	65.7	1215	13	ADR85721	Adr85721 Aspergill
c	10	46	65.7	1326	13	ADR85134	Adr85134 Aspergill
c	11	46	65.7	7326	13	ADR84547	Adr84547 Aspergill
	12	46	65.7	13654	10	ADC86678	Adc86678 Human GPC
	13	46	65.7	47804	10	ADC86176	Adc86176 Human GPC
	14	45	64.3	292	8	ABX94157	Abx94157 Incyte ID
	15	45	64.3	299	8	ABX94156	Abx94156 Incyte ID
	16	45	64.3	299	10	AAD61596	Aad61596 Rat MAPOP
c	17	45	64.3	478	4	AAI85737	Aai85737 Human pol
	18	45	64.3	502	8	ABX94147	Abx94147 Incyte ID
	19	45	64.3	502	10	AAD61592	Aad61592 Rat MAPOP
c	20	45	64.3	520	12	ACH68088	Ach68088 Human gen
	21	45	64.3	548	8	ABX94148	Abx94148 Incyte ID
	22	45	64.3	577	8	ABX94149	Abx94149 Incyte ID
	23	45	64.3	586	4	AAK63266	Aak63266 Human imm
c	24	45	64.3	6063	2	AAQ37205	Aaq37205 Delta-ami
c	25	45	64.3	27007	4	AAS27764	Aas27764 DNA encod
c	26	45	64.3	27007	10	ADB94567	Adb94567 Novel hum
c	27	45	64.3	31477	11	ACN44096	Acn44096 Mouse gen
c	28	45	64.3	90400	12	ADP08389	Adp08389 Human chr
c	29	45	64.3	155937	12	ADQ19389	Adq19389 Human sof
c	30	44	62.9	350	5	ABV14442	Abv14442 Human pro
c	31	44	62.9	386	5	ABV35525	Abv35525 Human pro
c	32	44	62.9	386	5	ABV44336	Abv44336 Human pro
c	33	44	62.9	457	4	AAL12073	Aal12073 Human bre
	34	44	62.9	543	4	AAL01367	Aal01367 Human rep
	35	44	62.9	543	4	AAL05056	Aal05056 Human rep
	36	44	62.9	543	4	ABL97949	Abl97949 Human tes
	37	44	62.9	543	4	ABL96820	Abl96820 Human tes
c	38	44	62.9	605	13	ACN46253	Acn46253 Cotton pr
	39	44	62.9	607	13	ADQ52289	Adq52289 Novel can
	40	44	62.9	794	4	AAH05678	Aah05678 Human cDN
c	41	44	62.9	888	11	ACN82255	Acn82255 Breast ca
	42	44	62.9	1015	12	ADJ50940	Adj50940 Human cDN
	43	44	62.9	1188	12	ADJ50938	Adj50938 Human cDN
c	44	44	62.9	1242	4	ABL25337	Abl25337 Drosophil
	45	44	62.9	1566	10	ADE07579	Ade07579 Novel cod

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OM protein - protein search, using sw model

Run on: February 23, 2005, 06:02:22 ; Search time 23 Seconds
                                    (without alignments)
                                    50.200 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

```
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database  :      PIR_79:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	67.1	3839	2	T49799	related to TOM1 pr
2	42	60.0	312	2	G97162	hypothetical prote
3	42	60.0	381	2	F84615	hypothetical prote
4	42	60.0	1206	2	E86445	hypothetical prote
5	41	58.6	763	2	A47563	glucose-6-phosphat
6	41	58.6	934	2	T42394	potassium channel
7	41	58.6	962	2	I53197	potassium channel
8	41	58.6	989	2	I48912	potassium channel
9	41	58.6	1174	2	A40853	potassium channel
10	40	57.1	471	2	AC2014	two-component sens
11	40	57.1	1178	2	S44142	VLA-2 protein homo
12	39	55.7	537	2	I51592	protein-tyrosine k
13	38.5	55.0	172	2	T34413	hypothetical prote
14	38	54.3	320	2	T09288	late embryonic abu
15	38	54.3	746	2	T43648	probable sexual cy
16	38	54.3	1461	2	T13157	mitotic checkpoint
17	37	52.9	182	2	D70859	hypothetical prote
18	37	52.9	388	2	T06035	hypothetical prote
19	37	52.9	398	1	TVFVVR	transforming prote
20	37	52.9	676	2	A45984	sperm-binding glyc
21	37	52.9	782	2	T22134	hypothetical prote
22	36.5	52.1	965	2	T12545	hypothetical prote
23	36	51.4	130	2	G86804	cytidine deaminase
24	36	51.4	249	2	H71131	hypothetical prote
25	36	51.4	384	2	AG3494	recF protein [impo
26	36	51.4	408	2	S33683	site-specific DNA-
27	36	51.4	1611	2	T38236	hypothetical prote

```
28        36      51.4    1894    2   JC4980              plexin 1 precursor
29        36      51.4    2533    2   T28675              alpha-51D immobili
30        36      51.4    2533    2   T28674              alpha-51D-immobili
31        35.5    50.7     561    2   T11378              NADH2 dehydrogenas
32        35      50.0     131    2   AG3198              hypothetical prote
33        35      50.0     138    2   T48293              hypothetical prote
34        35      50.0     220    2   T30688              hypothetical prote
35        35      50.0     237    2   T24407              hypothetical prote
36        35      50.0     246    2   S74408              lipopeptide antibi
37        35      50.0     321    2   E97741              D-alanine-D-alanin
38        35      50.0     360    2   T35783              probable secreted
39        35      50.0     365    2   T43286              cet-1 protein - Ca
40        35      50.0     377    2   AD2922              altronate oxidored
41        35      50.0     377    2   E97696              altronate oxidored
42        35      50.0     379    2   T29518              hypothetical prote
43        35      50.0     432    2   T23762              hypothetical prote
44        35      50.0     461    2   T41369              hypothetical prote
45        35      50.0     466    2   F69331              conserved hypothet
```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 06:41:19 ; Search time 2133 Seconds
                                              (without alignments)
                                              214.145 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries .

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US10618336/runat_18022005_145630_15135/app_query.fasta_1.1
99
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

```
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10618336_@CGN_1_1_4352_@runat_18022005_145630_15135 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :      EST:*
                1:  gb_est1:*
                2:  gb_est2:*
                3:  gb_htc:*
                4:  gb_est3:*
                5:  gb_est4:*
                6:  gb_est5:*
                7:  gb_est6:*
                8:  gb_gss1:*
                9:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	75.7	838	8	BZ200466	BZ200466 CH230-445
c 2	53	75.7	1721	3	BC045753	BC045753 Homo sapi
3	52	74.3	560	8	BZ109194	BZ109194 CH230-158
4	51	72.9	753	4	BI116555	BI116555 602868601
5	50	71.4	713	9	CG132573	CG132573 PUIIS63TB
c 6	50	71.4	868	9	CG100176	CG100176 PUFSZ03TB
7	50	71.4	873	9	CG100178	CG100178 PUFSZ03TD
c 8	50	71.4	945	8	CC195750	CC195750 ZMMBBc031
9	49	70.0	175	9	CE305331	CE305331 tigr-gss-
c 10	49	70.0	290	8	BZ857894	BZ857894 CH240_206
11	49	70.0	396	6	CB773497	CB773497 AMGNNUC:N
12	49	70.0	408	8	BH110778	BH110778 RPCI-24-3
13	49	70.0	513	8	BZ300561	BZ300561 KD0792.R1
14	49	70.0	607	9	CR177418	CR177418 Reverse s
15	49	70.0	705	9	AG301037	AG301037 Mus muscu
16	49	70.0	724	9	AG119495	AG119495 Pan trogl
17	49	70.0	736	9	AG565506	AG565506 Mus muscu
18	49	70.0	759	8	AZ254101	AZ254101 RPCI-23-6
19	49	70.0	1013	5	BU262687	BU262687 603820370
20	49	70.0	2320	3	BC036311	BC036311 Homo sapi
c 21	48	68.6	397	1	AI023232	AI023232 ov78e02.s
c 22	48	68.6	480	8	BZ408900	BZ408900 OGABS66TM
23	48	68.6	493	8	BZ408892	BZ408892 OGABS66TC
c 24	48	68.6	514	2	BF261235	BF261235 1M0003B06
c 25	48	68.6	659	2	BE973830	BE973830 601680637
c 26	48	68.6	770	9	CE024478	CE024478 tigr-gss-
c 27	48	68.6	785	8	AZ046018	AZ046018 nbeb0088J
c 28	48	68.6	881	4	BI099923	BI099923 602885050
29	48	68.6	1040	4	BM466654	BM466654 AGENCOURT
c 30	47	67.1	264	2	AW428085	AW428085 64905 MAR

```
c 31      47    67.1    277  1  AT003318          AT003318 AT003318
c 32      47    67.1    282  9  CG943500          CG943500 MBEAX54TR
c 33      47    67.1    406  8  AZ650391          AZ650391 1M0520J01
  34      47    67.1    408  5  BP938592          BP938592 25-026-P1
  35      47    67.1    460  8  AZ015845          AZ015845 RPCI-23-3
c 36      47    67.1    469  4  BI680462          BI680462 458735 MA
  37      47    67.1    508  8  AZ075000          AZ075000 RPCI-23-4
c 38      47    67.1    529  6  CA290583          CA290583 SCUTSD102
  39      47    67.1    571  5  BU108507          BU108507 603110129
  40      47    67.1    586  5  BQ556552          BQ556552 H4040G08-
c 41      47    67.1    662  4  BI078115          BI078115 602872423
c 42      47    67.1    712  9  CNS01TAE          AL166271 Tetraodon
  43      47    67.1    718  7  CN839615          CN839615 AGENCOURT
  44      47    67.1    728  5  BP437710          BP437710 BP437710
c 45      47    67.1    745  6  CD854754          CD854754 DH0AMM34Z
```

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OM protein - protein search, using sw model

Run on: February 23, 2005, 05:23:53 ; Search time 77 Seconds
                                        (without alignments)
                                        79.805 Million cell updates/sec

Title: US-10-618-336-6
Perfect score: 70
Sequence: 1 MCPTDMPASLCM 12

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                   1: uniprot_sprot:*
                   2: uniprot_trembl:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                               SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB ID   Description

1	47	67.1	4065	1	TOM1_NEUCR	Q9p4z1	neurospora
2	44	62.9	121	2	Q9H7W8	Q9h7w8	homo sapien
3	44	62.9	365	2	Q8IV13	Q8iv13	homo sapien
4	42	60.0	312	1	MRAW_CLOAB	Q97h81	clostridium
5	42	60.0	381	2	Q8LA81	Q8la81	arabidopsis
6	42	60.0	381	2	Q9ZQ45	Q9zq45	arabidopsis
7	42	60.0	1206	2	Q9FVQ7	Q9fvq7	arabidopsis
8	41	58.6	27	2	Q81172	Q81172	hepatitis b
9	41	58.6	204	2	Q986U1	Q986u1	rhizobium l
10	41	58.6	278	2	Q6Z2H6	Q6z2h6	oryza sativ
11	41	58.6	297	2	Q7QNM1	Q7qnm1	anopheles g
12	41	58.6	543	2	Q9W645	Q9w645	gallus gall
13	41	58.6	568	2	Q847W2	Q847w2	vibrio para
14	41	58.6	599	2	Q87PX3	Q87px3	vibrio para
15	41	58.6	763	1	G6PE_RABIT	P56201	oryctolagus
16	41	58.6	956	2	O44164	O44164	caenorhabdi
17	41	58.6	956	2	Q9XYX7	Q9xyx7	caenorhabdi
18	41	58.6	962	1	KCH1_RAT	Q63472	rattus norv
19	41	58.6	987	1	KCH1_BOVIN	O18965	bos taurus
20	41	58.6	988	1	KCH5_HUMAN	Q8ncm2	homo sapien
21	41	58.6	988	1	KCH5_RAT	Q9epi9	rattus norv
22	41	58.6	988	2	Q6NZH0	Q6nzh0	mus musculu
23	41	58.6	988	2	Q8C035	Q8c035	mus musculu
24	41	58.6	989	1	KCH1_HUMAN	O95259	homo sapien
25	41	58.6	989	1	KCH1_MOUSE	Q60603	mus musculu
26	41	58.6	1007	2	Q7QCM9	Q7qcm9	anopheles g
27	41	58.6	1011	2	Q7YW98	Q7yw98	manduca sex
28	41	58.6	1174	1	CIKE_DROME	Q02280	drosophila
29	41	58.6	1174	2	Q9VXZ6	Q9vxz6	drosophila
30	41	58.6	1285	2	Q8JUV1	Q8juv1	avian reovi
31	40	57.1	323	2	Q8CB84	Q8cb84	mus musculu
32	40	57.1	471	2	Q8YWE8	Q8ywe8	anabaena sp
33	40	57.1	508	1	VL1_HPV60	P50821	human papil
34	40	57.1	1178	1	ITA2_MOUSE	Q62469	mus musculu
35	40	57.1	1178	2	Q6P1C7	Q6p1c7	mus musculu
36	40	57.1	2116	2	Q6D9Y1	Q6d9y1	erwinia car
37	40	57.1	2168	2	Q6LGA3	Q6lga3	photobacter
38	39	55.7	196	2	Q6Y2V5	Q6y2v5	desulfuromo
39	39	55.7	198	2	Q8LF87	Q8lf87	arabidopsis
40	39	55.7	222	2	Q9LT60	Q9lt60	arabidopsis
41	39	55.7	264	2	Q66IP2	Q66ip2	xenopus lae
42	39	55.7	300	2	Q9YUQ5	Q9yuq5	turkey aden
43	39	55.7	318	2	Q67Q57	Q67q57	symbiobacte
44	39	55.7	328	2	Q8LJD0	Q8ljd0	oryza sativ
45	39	55.7	346	2	Q652V2	Q652v2	oryza sativ